6. (Amended) A method for detecting an increased risk of developing a neural tube defect, Down's Syndrome, or cardiovascular disease in a mammalian embryo or fetus, said method comprising detecting the presence of a polymorphic methionine synthase reductase (MTRR) in a test subject, wherein said test subject is a future parent of said embryo or said fetus, and wherein detection of a homozygous MTRR polymorphism in said future parent, said embryo, or said fetus, or detection of either a homozygous or heterozygous MTRR polymorphism in both future parents indicates an increased risk of developing said neural tube defect, Down's Syndrome, or cardiovascular disease in said embryo or said fetus, wherein said polymorphism comprises

(a) a G instead of an A at position 66 relative to the first nucleotide of the start codon of MTRR,

(b) a G instead of an A at position 110 relative to the first nucleotide of the start codon of MTRR,

(c) a deletion of 4 nucleotides starting from position 1675 (nucleotides 1675-1678) relative to the first nucleotide of the start codon of MTRR, or

(d) a deletion of 3 nucleotides starting from nucleotide 1726 (nucleotides 1726-1728) relative to the first nucleotide of the start codon of MTRR.

7. (Amended) The method of claim 6 or 35, wherein said polymorphic MTRR is detected by analyzing nucleic acid from said test subject.

21. (Amended) The method of claim 6 or 35, wherein said cardiovascular disease is premature coronary artery disease.

Add the following new claims 35-41.

35. (New) A method for detecting an increased risk of Down's Syndrome, hyperhomocysteinemia, cardiovascular, or cancer in a mammal, said method comprising

detecting the presence of a homozygous MTRR polymorphism that indicates an increased risk of Down's Syndrome, hyperhomocysteinemia, cardiovascular, or cancer in said mammal, wherein said polymorphism comprises

(a) a G instead of an A at position 66 relative to the first nucleotide of the start codon of MTRR,

(b) a G instead of an A at position 110 relative to the first nucleotide of the start codon of MTRR,

(c) a deletion of 4 nucleotides starting from position 1675 (nucleotides 1675-1678) relative to the first nucleotide of the start codon of MTRR, or

(d) a deletion of 3 nucleotides starting from nucleotide 1726 (nucleotides 1726-1728) relative to the first nucleotide of the start codon of MTRR.

36. (New) The method of claim 6, wherein said test subject is human.

37. (New) The method of claim 35, wherein said mammal is human.

38. (New) The method of claim 6, further comprising measuring the level of cobalamin in said test subject.

39. (New) The method of claim 35, further comprising measuring the level of cobalamin in said mammal.

40. (New) The method of claim 6, wherein said polymorphism comprises a G instead of an A at position 66 of MTRR.

41. (New) The method of claim 35, wherein said polymorphism comprises a G instead of an A at position 66 of MTRR.